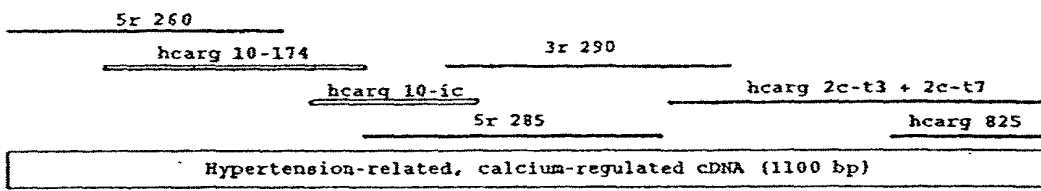


A



B

-131 SCACGAGCCACAGCCAGCTACCGGGCTAGGTTCTCCAGGTGCAGAGGGCG -80
 GTAAAGSCTTGGTTTGTATTTGTAATGCAACTGTGGTTAGGACCTTCTCTCGGACTGGTCAAGAAACGGGAAGAAAGG -1
 ATG TCT GCT TTG GGG GCT GCA GCT CCA TAC TTG CAC CAT CCC GCT GAC AGT CAC AGT GGC 60
 Met Ser Ala Leu Gly Ala Ala Ala Pro Tyr Leu His His Pro Ala Asp Ser His Ser Gly
 CGG GTC AGT TTC CTG GGT TCC CAG CCC TCT CCA GAA GTG ACG GCC GTG GCT CAG CTC TTG 120
 Arg Val Ser Phe Leu Gly Ser Gln Pro Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu
 AAG GAC TTA GAC AGG AGC ACC TTC AGA AAG TTG TTG AAA CTT GTA GTC GGG GCC CTG CAT 180
 Lys Asp Leu Asp Arg Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His
 GGG AAA GAC TGC AGA GAA GCT GTG GAG CAA CTT GCT GCC AGC GCC AAC CTG TCA GAA GAG 240
 Gly Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu
 CGT CTG GCC GTC CTG CTG GCG GCC ACA CAC ACC CTG CTC CAG CAG GCT CTC CGG CTG CCC 300
 Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala Leu Arg Leu Pro
 CCT GCT AGT CTA AAG CCA GAT GCC TTC CAG GAA GAG CTC CAG GAA CTT GGC ATT CCT CAG 360
 Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Glu Leu Gln Glu Leu Gly Ile Pro Gln
 GAT CTA ATT GGA GAT TTG GCC AGT TTG GCA TTT GGG AGT CAA CGC CCT CTT CTC GAC TCT 420
 Asp Leu Ile Gly Asp Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser
 GTA GCC CAA CAG CAG GGA TCC TCG CTG CCT CAC GTG TCT TAC TTC CGG TGG CGG GTG GAC 480
 Val Ala Gln Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp
 GTG GCC ATC TCA ACC AGC GCT CAG TCC CGC TCC CTG CAA CCG AGT GTT CTC ATG CAG CTG 540
 Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val Leu Met Gln Leu
 AAG CTC ACA GAT GGA TCT GCA CAC CGC TTC GAG GTG CCC ATA GCC AAA TTT CAG GAG CTG 600
 Lys Leu Thr Asp Gly Ser Ala His Arg Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu
 CGG TAC AGT GTA GCC TTG GTC CTT AAG GAG ATG GCA GAA CTG GAG AAG AAG TGT GAG CGC 660
 Arg Tyr Ser Val Ala Leu Val Leu Lys Glu Met Ala Glu Leu Glu Lys Lys Cys Glu Arg
 AAA CTG CAG GAC TGA CTGAACCTGGTACTGTGGGTGCTGAAGCTGGTACCAGAACACAGCCCCCACTGGTGA 734
 Lys Leu Gln Asp TER
 TGAGCCCAACTCCATTGAGGTCTTGCACTGTGAGAACGTTATTTAAGTGAAAAGACAGCGGGACTTTTCAGGTTTTGTTTT 813
 ATGACTCAACAGCTGGGCAGGTGGCACAGTTTATAATCTCAGCCCTTGGAAAGTCTGAGGCTGGAGAATGGGAAGTGTA 892
 AGCTGGGCCTGGCTTTCATAGTGAGGCTCAGTGTGCAATTAAAGAGGTAAAGCAACTATTAAAAA 969

FIGURE 1

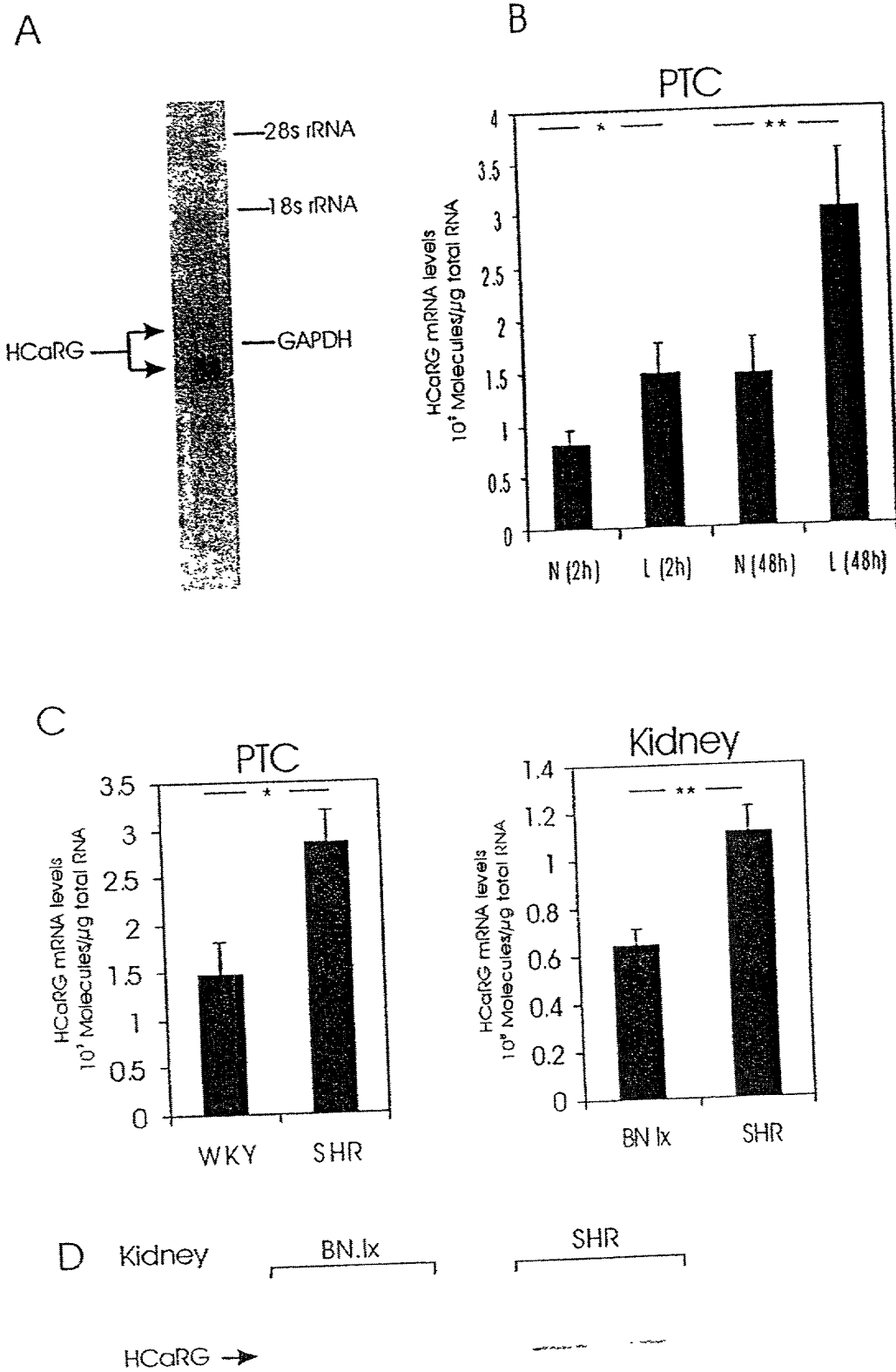


FIGURE 2

09904568-042502
205270-89540660

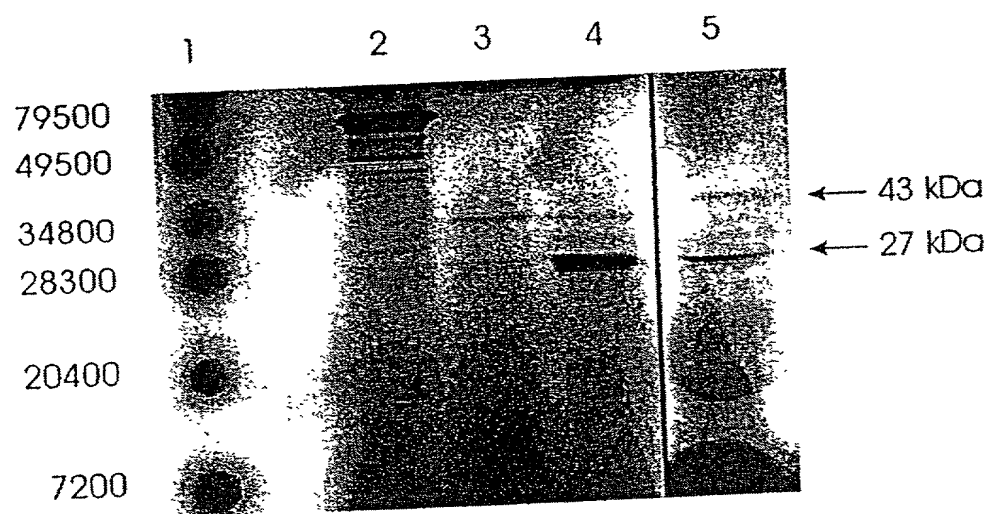


FIGURE 3

rHcARG	MSA	LGAAAPN	LDHHADG	LDHSGSOPS	PEVIAAQLI	KDLDRTFRK	50
hHcARG	MSA	LGAAATEY	LDHFGDSHSC	LDHSGRQLP	PEVIAARILL	GDLDRTFRK	50
rHcARG	LLK	LVVGAH	SGDCREAVIQ	LGASANTISEE	RLAVILAGTH	TTLGQAWRLP	100
hHcARG	LLK	FVSSIQ	GEDCREAVQR	LGVSANTISEE	QLGALLAGMH	TLEQCAHRLP	100
rHcARG	PAS	LKPDAR	EQEELQELGIPQ	DINGDLASLA	FGSORPLIDS	VAQQQSSLP	150
hHcARG	PAS	LKPDIFR	DQEQELGIPQ	DINGDLASVV	FGSORPLIDS	VAQQQGAWLP	150
rHcARG	HVS	YFRWRVD	VAISTSAQSR	SLQPSVLMQL	KLTGSAHFR	EVETAKFOEL	200
hHcARG	HVA	DFRWRVD	VAISTSALAR	SLQPSVLMQL	KLTGSAHFR	EVETAKFOEL	200
rHcARG	RYS	VALVLKE	MAELEKKCER	KLQD			224
hHcARG	RYS	VALVLKE	MAELEKKCER	KLQD			224

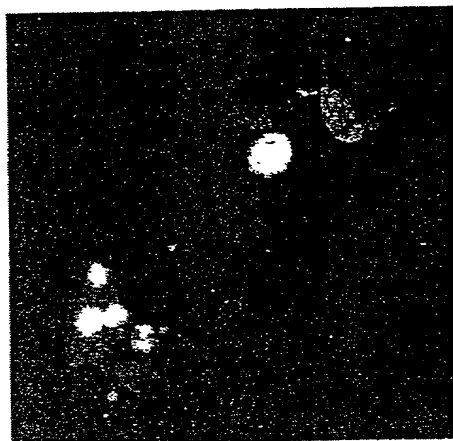
FIGURE 4

205240" 89540660

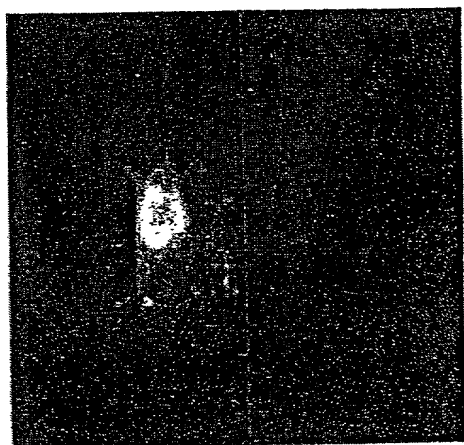
A



B



C



D

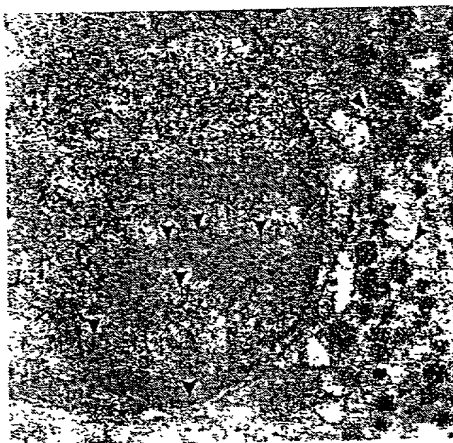


FIGURE 5

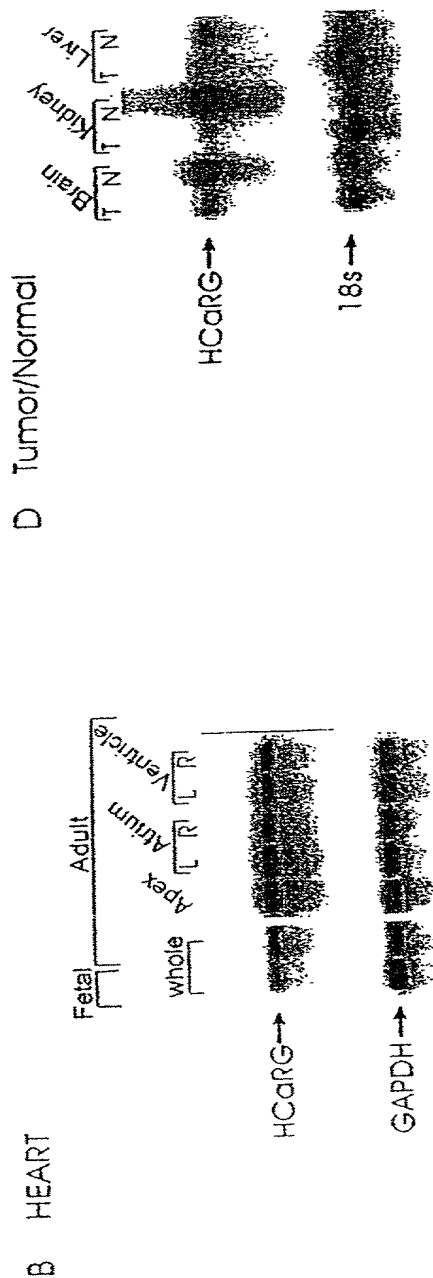
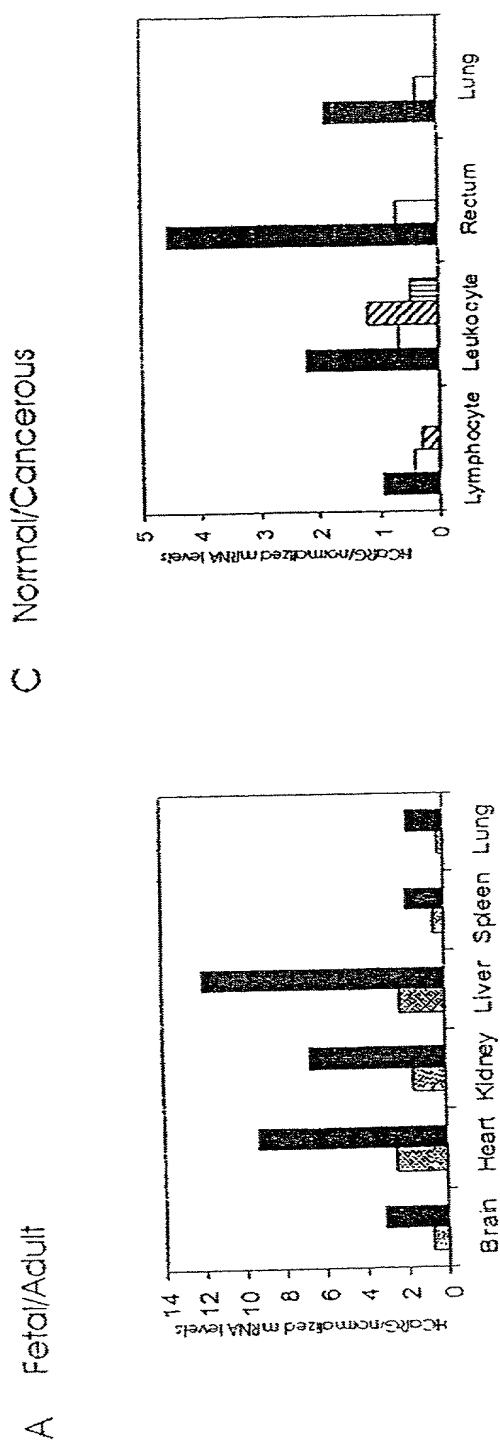


FIGURE 6

205240 89540660 0904568 042502

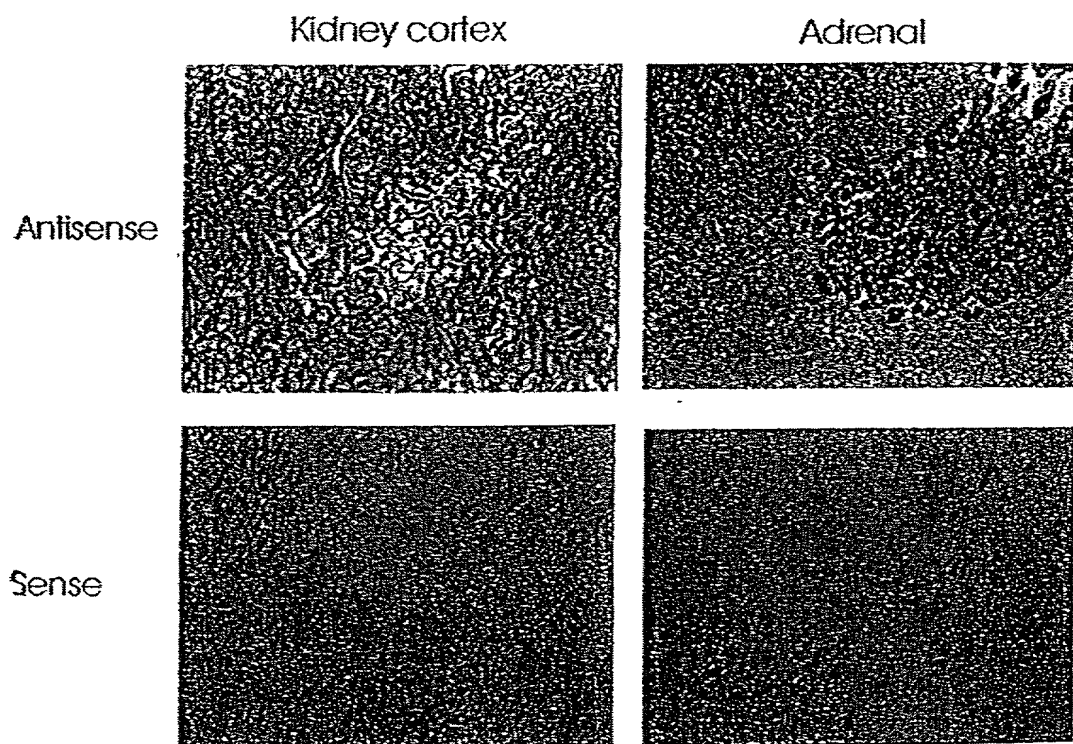
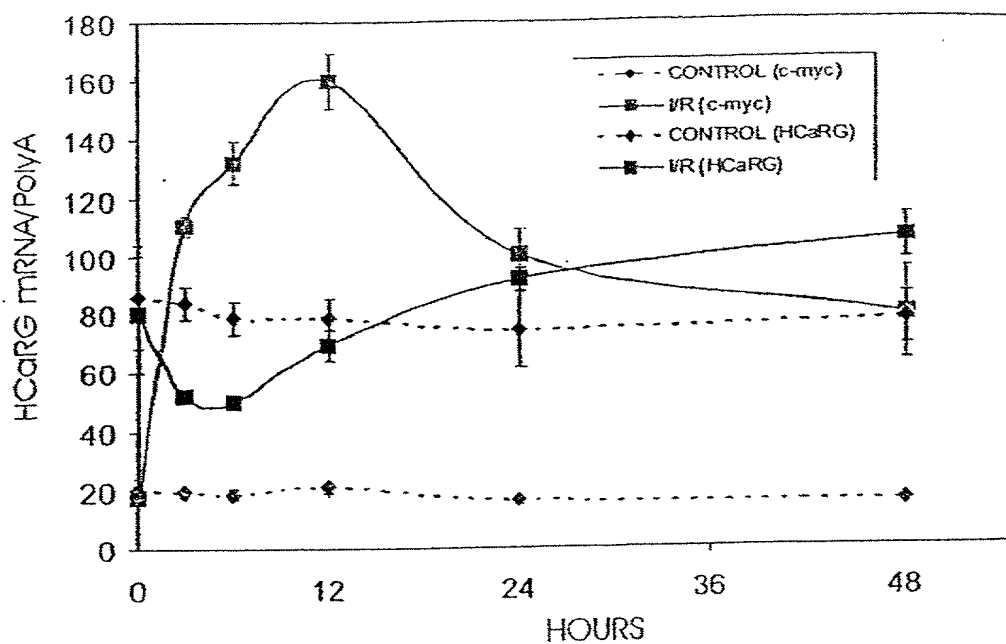
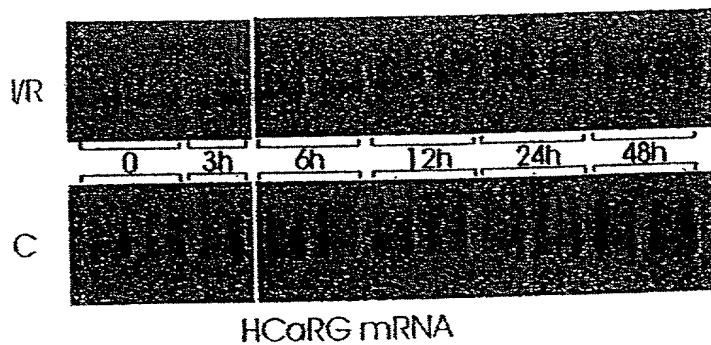


FIGURE 7

A Medulla



B Cortex



C Cortex

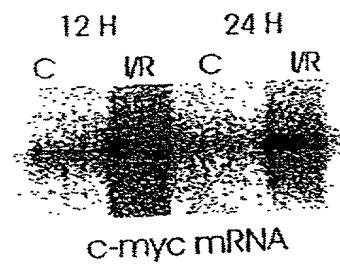
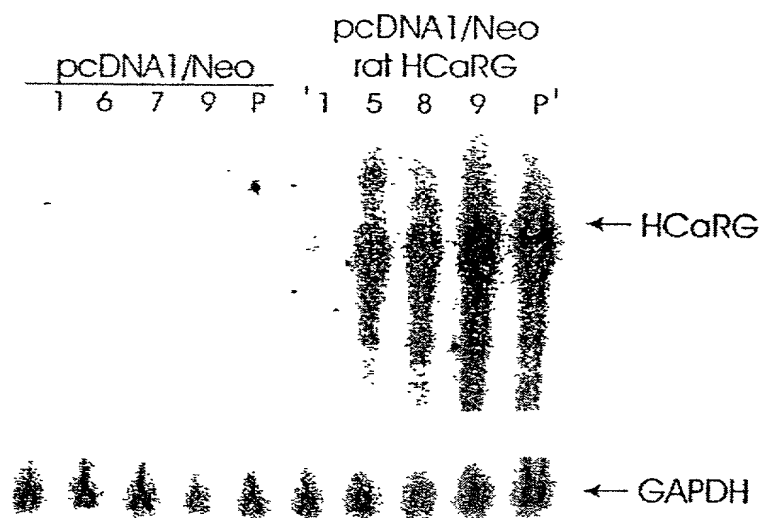


FIGURE 8

A



B

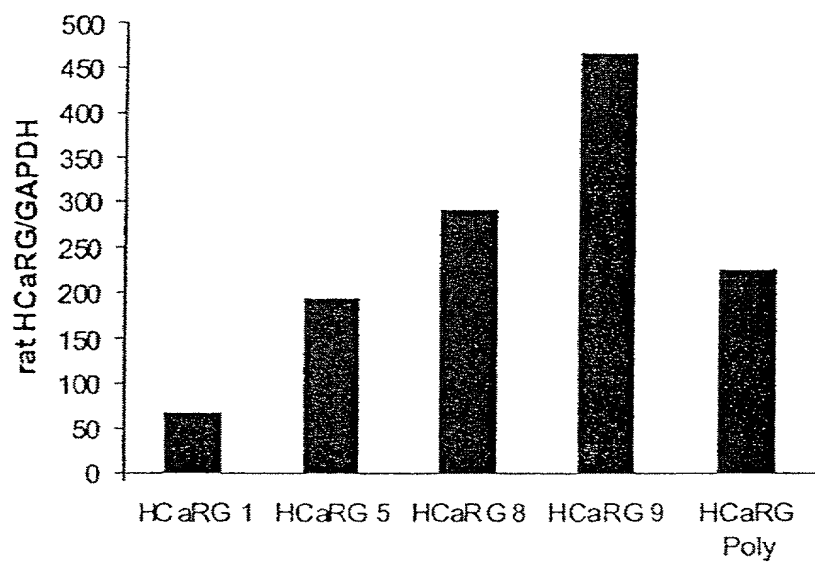
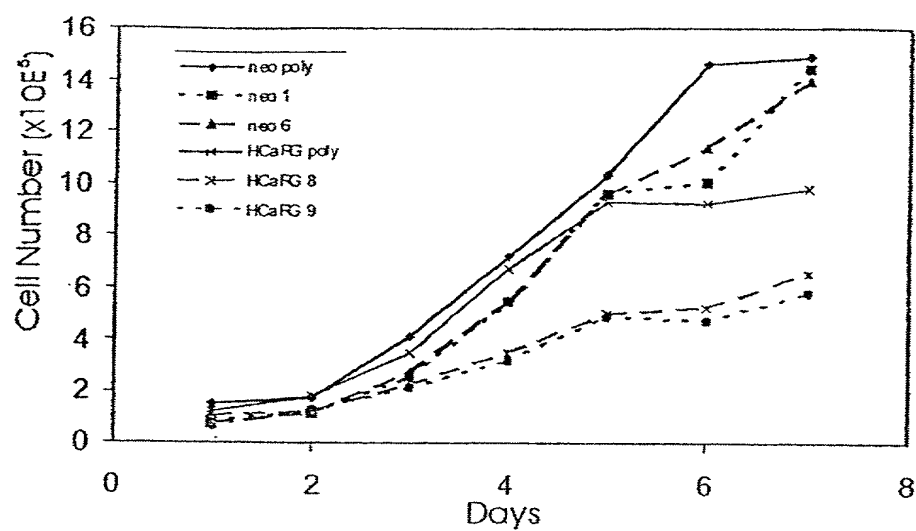


FIGURE 9

A



B

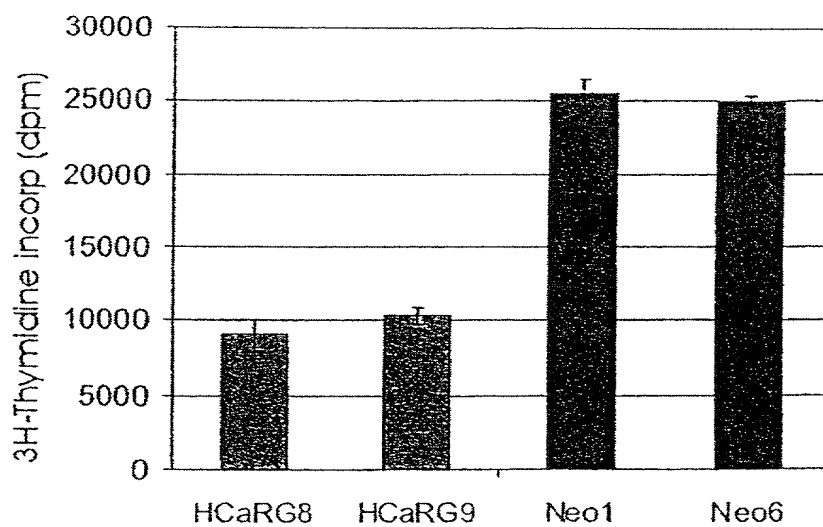


FIGURE 10

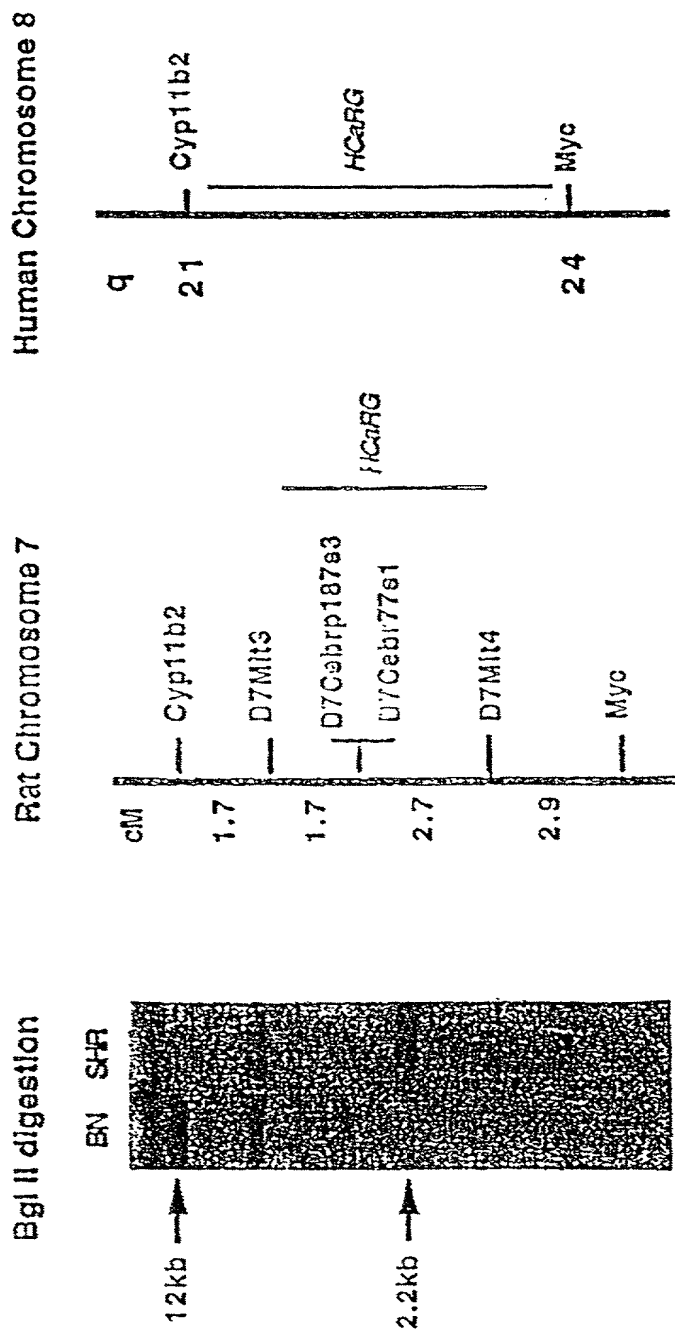


FIGURE 11